

O'Bryen, Barbara

From: Seharaseyon, Jegatheesan
Sent: Friday, February 28, 2003 5:46 PM
To: O'Bryen, Barbara
Subject: Re:Comparison

Importance: High

Hi Barb,

If you have not done the comparson please do so for the following SEQ ID NO: 1 of 08/828,922 (Patent NO;5,834,240) vs. SEQ ID NO; 2 of 09/856,836. Sorry I gave the wrong seq ID earlier. Thanks a lot.

Seyon.

J.Seharaseyon

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BSPB
3-3-03

> O <
> I O < Intelligence

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-08-828-922-1.res made by bobryen on Mon 3 Mar 103 9:21:48-PST.

Query sequence being compared: US-08-828-922-1 (1-350)
Number of sequences searched: 1
Number of scores above cutoff: 1

Results of the initial comparison of US-08-828-922-1 (1-350) with:
File: US09856836.pep

100-
N -
U 50-
M -
B -
E -
R -
O -
F 10-
S -
O 5-
Q -
U -
N -
C -
E -
S 0-
SCORE 0 37 74 111 148 185 222 259 296 333
STDY

PARAMETERS

Similarity matrix PAM-150 K-tuple 1
Threshold level of sim. 168
Mismatch penalty 1
Gap penalty 5.00 Joining penalty 20
Gap size penalty 0.05 Window size 350
Cutoff score 1
Randomization group 0

SEARCH STATISTICS

Scores: Mean 333 Median 0 Standard Deviation 0.00
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00

Number of residues: 351
Number of sequences searched: 1
Number of scores above cutoff: 1

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name Description Length Score Score Init. Opt. Sig. Frame

1. US-09-856-836-2 Sequence 2, Application US 351 333 339 0.00 0

1. US-08-828-922-1 (1-350)
US-09-856-836-2 Sequence 2, Application US/09856836

Initial Score = 333 Optimized Score = 339 Significance = 0.00
Residue Identity = 96% Matches = 337 Mismatches = 9
Gaps = 1 Conservative Substitutions = 4

X MEMQPTLTCGHTRPVVDLAFSGITPYGFFLISACKDGPMLRGDGTGDMIGTFLGKGAWGATLNDAT
MAMQPTLTCGHTRPVVDLAFSGITPYGFFLISACKDGPMLRGDGTGDMIGTFLGKGAWGATLNDAT
X 10 20 30 40 50 60 70

KAATAADFTAKYWDVAVSGDELMTLAKHIVKTVDFDODSNYLLTGQDKLLRIYDLNKPAPAPKESIGHTS
KAATAADFTAKYWDVAVSGDELMTLAKHIVKTVDFDODSNYLLTGQDKLLRIYDLNKPAPAPKESIGHTS
X 80 90 100 110 120 130 140

GIRKALMCSDDKOILSADDKTYVLMHATVTEKSLNFMNVSMSMETIEGELIVYTGGRSIAFHSVSLDP
GIRKALMCSDDKOILSADDKTYVLMHATVTEKSLNFMNVSMSMETIEGELIVYTGGRSIAFHSVSLDP
X 150 160 170 180 190 200 210

IKSEFAPATINSASLHPEKEFLVAGGEDFKLYKIDYNSGEELBSTYKGFHCVRFSPDGLYASGEDGT
IKSEFAPATINSASLHPEKEFLVAGGEDFKLYKIDYNSGEELBSTYKGFHCVRFSPDGLYASGEDGT
X 220 230 240 250 260 270 280

LRLMOTVYKRTYGLMKCVLPEDDSGELAPKIGFPTTPEEL-ETIASNSDCIPSPADVKA
LRLMOTVYKRTYGLMKCVLPEDDSGELAPKIGFPTTPEEL-ETIASNSDCIPSPADVKA
X 290 300 310 320 330 340 350